

REMARKS

Claims 1-3, 6, 7, 16, 17 and 19-29 are pending; claims 3 and 24 are allowed; claims 1, 2, 6, 7, 16, 17, 19-23 and 25-29 are rejected.

After entry of this amendment, claims 1-3, 16, 17, 19-22 and 24 will be pending.

No new matter has been added. Entry of this amendment is respectfully requested.

I. Formal Matters

At page 2 of the Office Action, under "Sequence Rules", the Examiner indicates that the diskette containing the electronic version of the Sequence Listing filed December 31, 2003, was misplaced by the U.S. PTO, and requests that a copy be filed.

However, as stated in a further Office communication, dated December 9, 2004, the Examiner has now located the diskette. Therefore, Applicants believe that no action is required.

II. Rejection of Claims Under 35 U.S.C. §102

At page 3 of the Office Action, claims 2, 6, 7 and 19 remain rejected, and new claims 23, 27 and 28 are also rejected, under 35 U.S.C. §102(b), as being anticipated by GenEmbl accession number Y11416 (Sept. 2, 1997) as evidenced by Kaghad et al. (1997).

The Examiner states that claims 2, 6 and 7 are anticipated because the protein coding region of Y11416 has about 70% sequence homology to the protein coding region of SEQ ID NO:2 of the instant application. The Examiner further states that it is the position of the U.S. PTO that two sequences having 70% sequence homology over more than 1 kb would hybridize under the specified conditions.

The Examiner states that the phrase "a few amino acids" recited in claims 23, 27 and 28 is not defined as having a maximum limit in the specification, and therefore the claims are

anticipated by the polypeptide of Y11416 that encodes a protein having about 72% homology to the polypeptide of SEQ ID NO:1.

Claims 6, 7 23, 27 and 28 have been canceled, thus rendering moot the rejection as to these claims.

Claim 2 is herein amended to recite hybridizing polynucleotides that have “apoptosis inducing activity.” The polypeptide of Y11416, as described in Kaghad et al., does not have such activity. Indeed, at discussed at page 814, col. 2, first paragraph of Kaghad et al., the polypeptide of Y11416 is thought to be a transcription factor. Therefore, neither Y11416 nor Kaghad et al., alone or in combination, teaches each element of claim 2, and thus does not anticipate claim 2. For the same reasons, the cited art does not anticipate dependent claim 19.

In view of these comments and the amendments to the claims, Applicants respectfully request reconsideration and withdrawal of the rejection.

III. Rejection of Claims Under 35 U.S.C. §112

A. At page 5 of the Office Action, claims 21, 23 and 25-29 are rejected under 35 U.S.C. §112, second paragraph, as being indefinite.

Claim 21

The Examiner states that while claim 21 recites the limitation “the DNA binding domain” in line 6, there is insufficient antecedent basis for this term.

Included herewith is an amendment to claim 21 such that the claim recites “a DNA binding domain” in place of “the DNA binding domain”.

Applicants respectfully assert that the claim is definite as written, and respectfully request reconsideration and withdrawal of this rejection.

Claims 23 and 25-29

Each of claims 23 and 25-29 has been canceled, thus making the rejection moot as to these claims.

B. At page 6 of the Office Action, claims 1, 16, 17 and 22 are rejected under 35 U.S.C. §112, first paragraph, as lacking adequate written description.

The Examiner notes that the claims are being rejected due to an introduction of new matter. The Examiner states that while claim 1 recites a polypeptide having 50% overall homology and homology to each of the three recited domains, the specification only provides support for a polypeptide having 50% homology or homology to one of the three recited domains.

Applicants respectfully disagree with the Examiner's position for the following reasons.

As stated in line 8, at page 27 of the specification, the degree of homology of the full-length sequence is preferably not less than 50%. Thus, there is clear support for a polypeptide with an overall homology of 50%.

Next, lines 12-21 (page 27) state that the homology should not be less than a given value in "at least one" of the transcriptional activation domain, DNA binding domain and oligomerization domain. This sentence does not state that the homology is in only one of the three domains, it states that the homology is in at least one of the domains. Because "at least one" can include all three of the domains, there is clear support for a polypeptide having homology to all three of the domains recited in the claims.

Finally, there is support for both of these limitations together in the same polypeptide, namely, a polypeptide having both an overall homology of at least 50%, and having homology to

all three of the domains recited in the claim. Line 12, at page 27, states that the polypeptide having homology to the three domains is a preferred version of the polypeptide having an overall homology of 50%. Therefore, by definition the polypeptide having homology to the three domains also has an overall homology of 50%. Thus, there is clear and sufficient support in the specification for the polypeptides as recited in the rejected claims.

In view of these comments Applicants respectfully contend that the claims have adequate written description support in the specification and no new matter is being introduced.

Accordingly, Applicants respectfully request reconsideration and withdrawal of this rejection.

IV. Conclusion

In view of the above, reconsideration and allowance of this application are now believed to be in order, and such actions are hereby solicited. If any points remain in issue which the Examiner feels may be best resolved through a personal or telephone interview, the Examiner is kindly requested to contact the undersigned at the telephone number listed below.

The USPTO is directed and authorized to charge all required fees, except for the Issue Fee and the Publication Fee, to Deposit Account No. 19-4880. Please also credit any overpayments to said Deposit Account.

Respectfully submitted,



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